FIGURE 1

MA61 - A part of the SCF E3 ubiquitin Ligase Complex

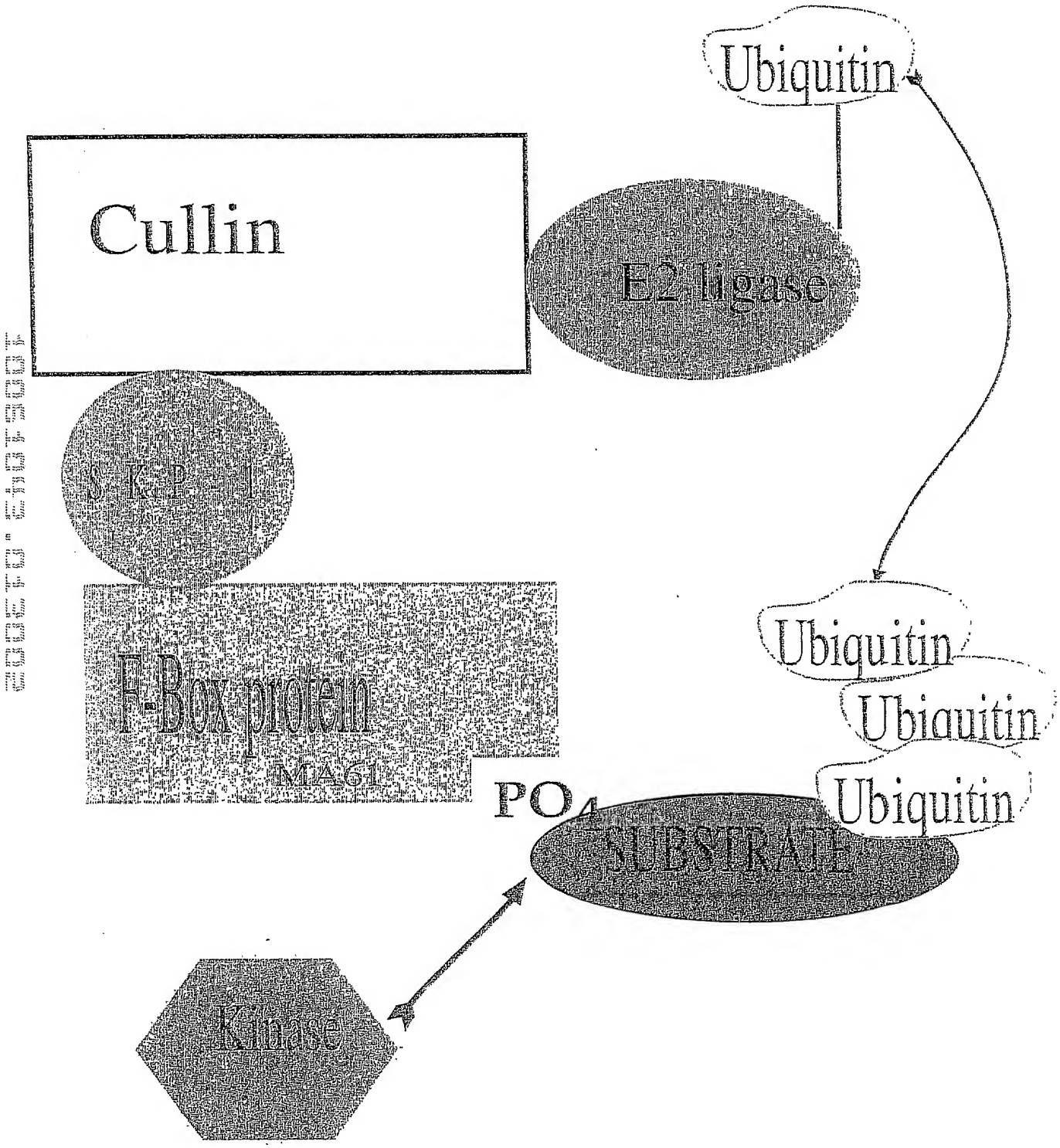


FIGURE 2

ClustalW Formatted Alignments

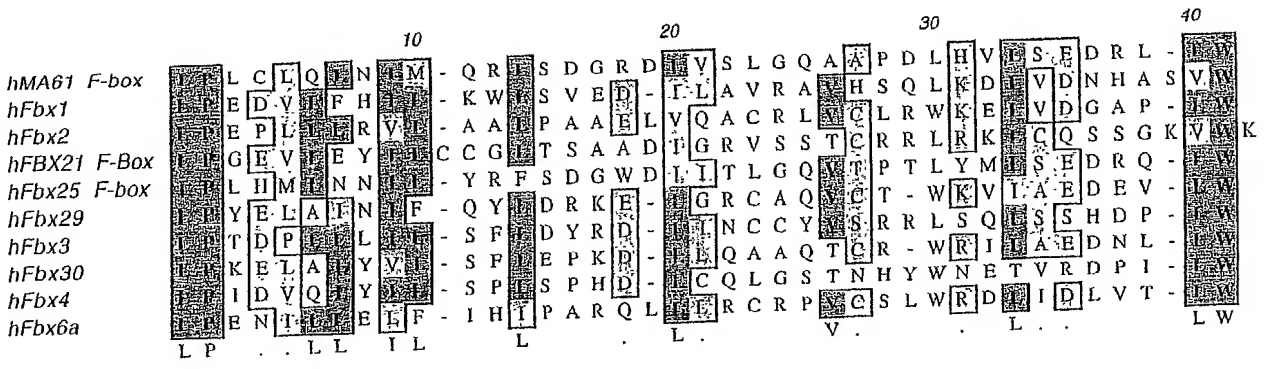
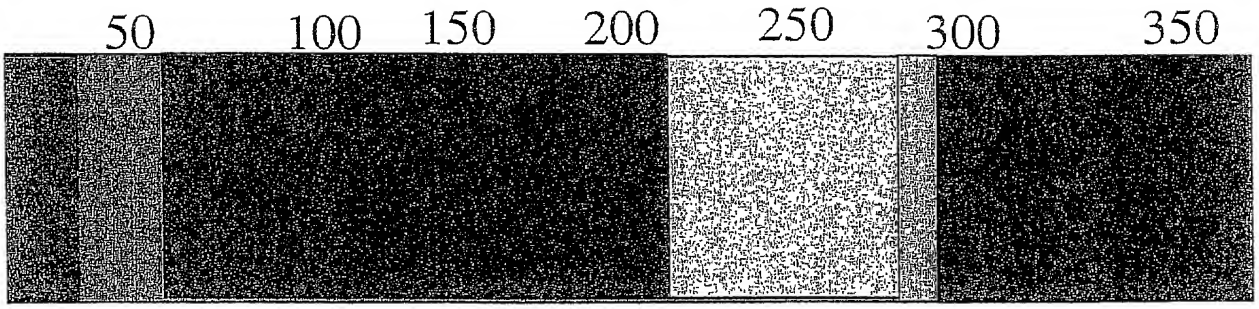


FIGURE 3

MA 61



Fbx25 Homology Domain (1-25; 86-360)

F-Box Domain (217-264)

Bipartite nuclear localization signal (262-279)

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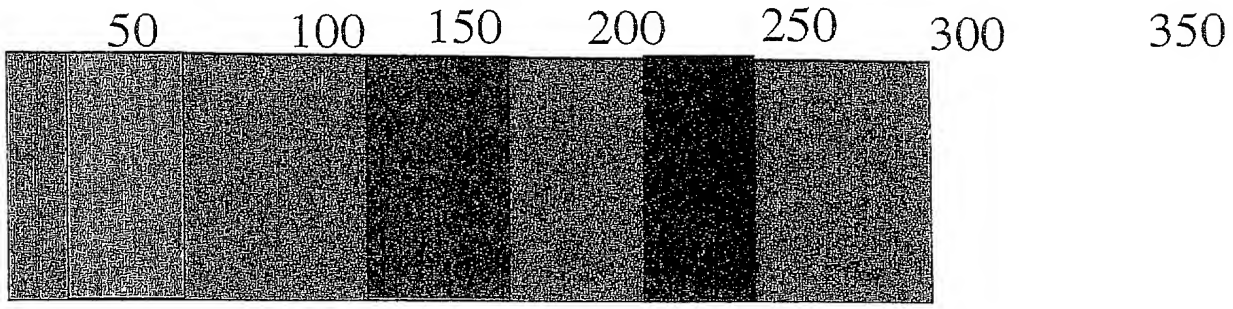
FIGURE 4

Human MURF 1 schematic



RING Finger Domain (26-82)

BBOX (121-163)

Spectrin Repeat (207-233)

20050707.070307

FIGURE 5A

ClustalW Formatted Alignments

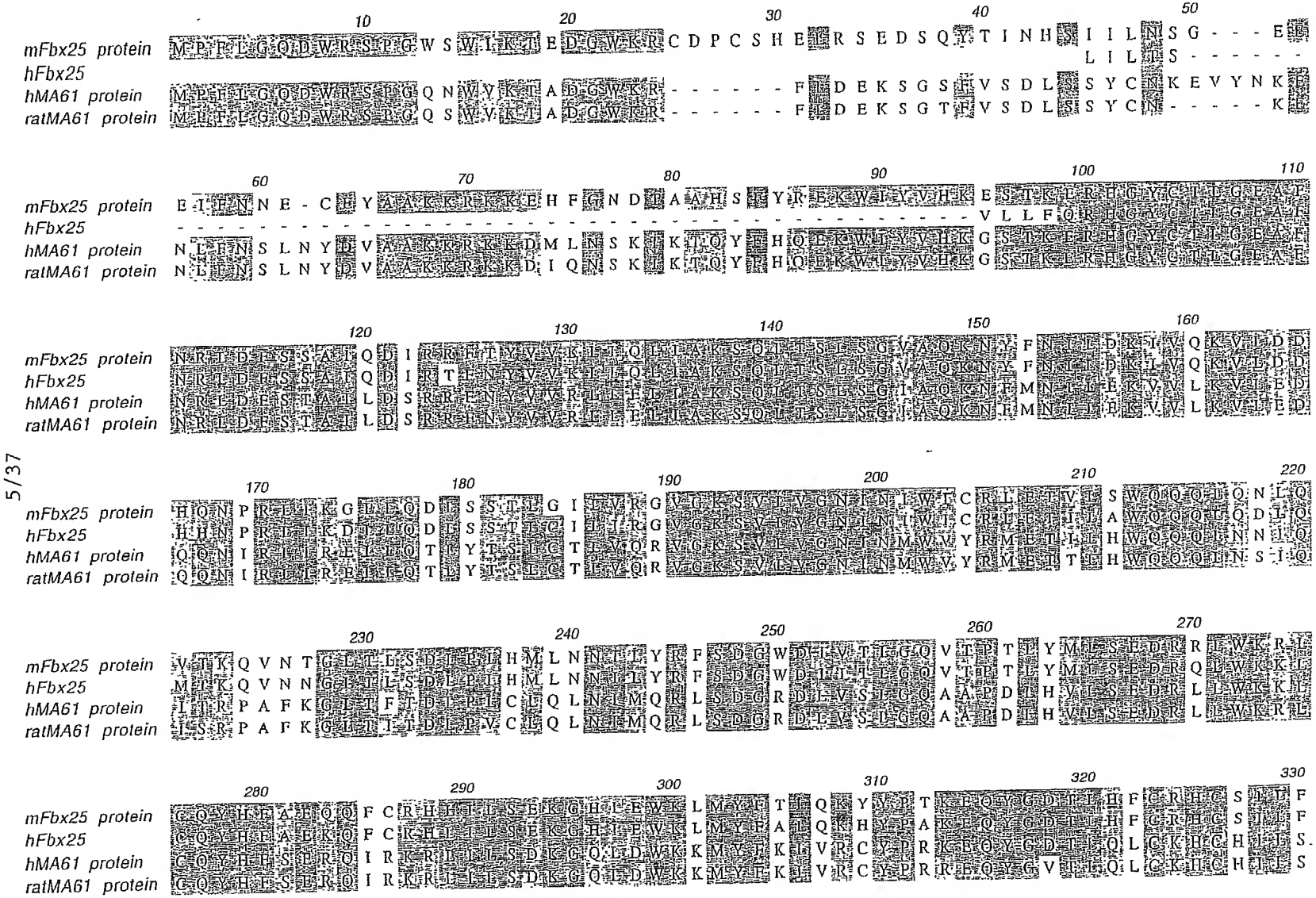


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FIGURE 5B

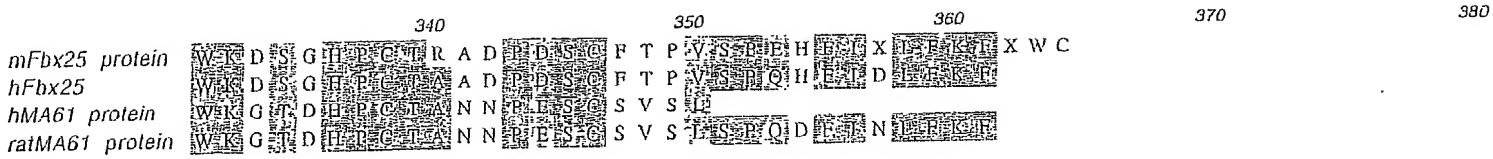

Figure 6

ATGGATTATAAATCTGGCTTGATTCCGGACGGAAATGCTATGGAGAACCTGG
AGAAGCAGCTCATCTGCCCCATCTGCCTTGAGATGTTTACCAAGCCTGTGGT
CATCCTGCCCTGCCAGCACAACCTCTGCCGGAAGTGTGCCAACGACATCTTC
CAGGCTGCCAATCCCTACTGGACCAACCGCGGTGGCTCGGTGTCCATGTCTGG
AGGTCGTTTCCGCTGCCCCTCGTGCCGCCATGAAGTGATCATGGACCGGCATG
GGGTGTACGGTCTGCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTA
CAAGCAGGAATGCTCCAGTCGGCCCCTGCAGAAAGGCAGCCACCCGATGTGC
AAGGAACACGAAGACGAGAAAATCAACATCTACTGTCTCACGTGCGAGGTG
CCTACTTGCTCCTTGTGCAAGGTGTTCGGGGCTCACCAGGCCTGTGAAGTTGC
CCCCTTACAAAGCATCTTCCAAGGACAGAAGACTGAACTGAGCAATTGCAT
CTCCATGCTGGTGGCAGGGAACGACCGAGTTCAGACTATCATCTCGCAGCTG
GAGGACTCCTGCCGAGTGACCAAGGAAAACAGCCACCAGGTGAAGGAGGAA
CTGAGCCACAAGTTTGACGCCCTCTACGCCATCCTGGACGAGAAGAAGAGTG
AGCTGCTGCAGCGGATCACTCAGGAGCAGGAGGAGAAGCTGGACTTCATCGA
GGCCCTGATCCTCCAGTACCGAGAGCAGTTGGAAAAGTCGACCAAGCTTGTG
GAAACAGCCATCCAGTCCCTGGATGAGCCCGGAGGGGCCACCTTCCTCTTGA
GTGCCAAGCCGCTCATCAAGAGCATTGTAGAAGCTTCCAAGGGCTGCCAGCT
GGGGAAGACAGAACAAGGCTTTGAGAACATGGACTACTTTACTCTGAATTT
AGAACACATAGCAGAGGCCTTGAGGGCCATCGACTTTGGGACAGATGAGGAG
GAGGAGTTTACTGAAGAGGAGGAGGAGGAGGATCAAGAAGAGGGCGTGTCC
ACAGAGGGACACCAA

Figure 7

MDYKSGLIPDGNAMENLEKQLICPICLEMFTKPVVILPCQHNLCRKCANDIFQAAN
PYWTNRGGSVSMSGGRFRCPSCRHEVIMDRHGVYGLQRNLLVENIIDIYKQECSS
RPLQKGSHPMCKEHEDEKINIYCLTCEVPTCSLCKVFGAHQACEVAPLQSIFQGQ
KTELSNCISMLVAGNDRVQTIISQLEDSCRVTKENSHQVKEELSHKFDALYAILDE
KKSELLQRITQEQEEKLDFIEALILQYREQLEKSTKLVETAIQSLDEPGGATFLLSA
KPLIKSIVEASKGCQLGKTEQGFENMDYFTLNLEHIAEALRAIDFGTDEEEEFTEEE
EEEDQEEGVSTEGHQ

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Figure 8A

```
        10         20         30         40         50
TTCTCAGGTACTTTATCGGACCTCTCACATGGCTGCATGCCCAGAAATGT

        60         70         80         90        100
GATGATATTGTTGACAGCCTCTTCAAGGGTTTTGGTAGAACTGAGGGCAA

       110        120        130        140        150
AGGTTTCCTCTTTCTCAAAGGTATCTCCCACCTCTTCCCAAGCAGCAGCA

       160        170        180        190        200
AAGTTAGGCTGACCTCGTCTGTTATGTAAAGGATGCGTAGGGATGGGAGG

       210        220        230        240        250
GCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGTTTCCAT

       260        270        280        290        300
TTCCTGAGCGTCTGAGATGTTAGTATTAGTTAGTTTTGTTGTGAGTGTTA

       310        320        330        340        350
GAATTCGGGCACCAGGAGAAGGAAGCCAACAGGATCCGACCCGGTGTTTT

       360        370        380        390        400
GTGACAAAGGCAAGACCCCCAGGTCTACTTAGAGCAAAGTTAGTAGAGGA

       410        420        430        440        450
GGCAGCTAGGCGTGGCTCTCATTCCTTCCCACAGAATGGATTATAAGTCG

       460        470        480        490        500
AGCCTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGAT

       510        520        530        540        550
CTGCCCTATCTGCCTGGAGATGTTTACCAAGCCAGTGGTCATCTTGCCGT

       560        570        580        590        600
GCCAGCACAACCTGTGCCGGAAGTGTGCCAATGACATCTTCCAGGCTGCA

       610        620        630        640        650
AATCCCTACTGGACCAGCCGGGGCAGCTCAGTGTCCATGTCTGGAGGCCG

       660        670        680        690        700
TTTCCGCTGCCCCACCTGCCGCCACGAGGTGATCATGGATCGTCACGGAG

       710        720        730        740        750
TGTACGGCCTGCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTAC

       760        770        780        790        800
AAACAGGAGTGCTCCAGTCGGCCGCTGCAGAAGGGCAGTCACCCCATGTG

       810        820        830        840        850
CAAGGAGCACGAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGG

       860        870        880        890        900
TGCCCACCTGCTCCATGTGCAAGGTGTTTGGGATCCACAAGGCCTGCGAG

       910        920        930        940        950
GTGGCCCCATTGCAGAGTGTCTTCCAGGGACAAAAGACTGAACTGAATAA
```

Figure 8B

960 970 980 990 1000
CTGTATCTCCATGCTGGTGGCGGGGAATGACCGTGTGCAGACCATCATCA

1010 1020 1030 1040 1050
CTCAGCTGGAGGATTCCCGTCGAGTGACCAAGGAGAACAGTCACCAGGTA

1060 1070 1080 1090 1100
AAGGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGA

1110 1120 1130 1140 1150
GAAGAAAAGTGAGTTGCTGCAGCGGATCACGCAGGAGCAGGAGGAAAAGC

1160 1170 1180 1190 1200
TTAGCTTCATCGAGGCCCTCATCCAGCAGTACCAGGAGCAGCTGGACAAG

1210 1220 1230 1240 1250
TCCACAAAGCTGGTGGAAACTGCCATCCAGTCCCTGGACGAGCCTGGGGG

1260 1270 1280 1290 1300
AGCCACCTTCCTCTTGACTGCCAAGCAACTCATCAAAAGCATTGTGGAAG

1310 1320 1330 1340 1350
CTTCCAAGGGCTGCCAGCTGGGGAAGACAGAGCAGGGCTTTGAGAACATG

1360 1370 1380 1390 1400
GACTTCTTTACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCAT

1410 1420 1430 1440 1450
TGACTTTGGGACAGATGAGGAAGAGGAAGAATTCATTGAAGAAGAAGATC

1460 1470 1480 1490 1500
AGGAAGAGGAAGAGTCCACAGAAGGGAAGGAAGAAGGACACCAGTAAGGA

1510 1520 1530 1540 1550
GCTGGATGAATGAGAGGCCCCCAGATGCAGAGAGACTGGAGAGGGTGGGG

1560 1570 1580 1590 1600
AGGGGCCCAGCGGCCTTGGTGACAGGCCCAGGGTGGGAGGGGTCGGGGCC

1610 1620 1630 1640 1650
CCTGGAGGGGCAATGGGGAGGTGATGTCTTCTCTCTGCTCAGAGAGCAGG

1660 1670 1680 1690 1700
GACTAGGGTAGGACCCTCACCGCTGCGTCCAGCAGACACTGAACCAGAAT

1710 1720 1730 1740 1750
TGGAAACGTGCTTGAAACAATCACACAGGACACTTTTCTACATTGGTGCA

1760 1770 1780 1790 1800
AAATGGAATATTTTGTACATTTTTAAAATGTGATTTTTGTATATACTTGT

1810 1820 1830 1840 1850
ATATGTATGCCAATTTGGTGCTTTTTGTAAAGGAACTTTTGTATAATAAT

1860 1870 1880 1890 1900
GCCTGGTCGTTGGGTGACCTGCGATTGTCAGAAAGAGGGGAAGGAAGCCA

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Figure 8C

```
      1910       1920       1930       1940       1950
GGTTGATACAGCTGCCCACTTCCTTTCCTGAGCAGGAGGATGGGGTAGCA

      1960       1970       1980       1990       2000
CTCACAGGGACGATGTGCTGTATTTCAGTGCCTATCCCAGACATACGGGG

      2010       2020       2030       2040       2050
TGGTAACTGAGTTTGTGTTATATGTTGTTTTAATAAATGCACAATGCTCT

      2060       2070       2080       2090
CTTCCTGTTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

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Figure 9

MENLEKQLICPICLEMFTKPVVILPCQHNLCRKCANDIFQAANPYWTSRGSSVSM
SGGRFRCPTCRHEVIMDRHGVYGLQRNLLVENIIDIYKQECSSRPLQKGSHPMCK
EHEDEKINIYCLTCEVPTCSMCKVFGIHKACEVAPLQSVFQGQKTELNNCISMLV
AGNDRVQTIITQLEDSRRVTKENSHQVKEELSQKFDTLYAILDEKKSELLQRITQE
QEEKLSFIEALIQQYQEQLDKSTKLVETAIQSLDEPGGATFLLTAKQLIKSIVEASK
GCQLGKTEQGFENMDFFTLDLEHIADALRAIDFGTDEEEEEFIEEEDQEEEESTEG
KEEGHQ

Figure 10

ATGCCGTTCCTTGGTCAGGACTGGCGGTCCCCGGGCCAGAGCTGGGTGAAGAC
GGCGGACGGCTGGAAGCGCTTCTTGGATGAGAAAAGCGGCACCTTCGTGAGC
GACCTCAGCAGTTACTGCAACAAGGAGAATCTGTTCAACAGCCTGAACTAC
GATGTTGCAGCCAAGAAGAGAAAGAAAGACATACAGAACAGCAAAACCAA
AACTCAGTATTTCCATCAGGAGAAGTGGATCTATGTTCACAAAGGGAGTAC
TAAGGAGCGCCATGGATACTGCACTTTGGGGGAAGCTTTCAACAGACTGGAC
TTCTCGACTGCCATCCTGGATTCCAGAAGATTCAACTACGTAGTAAGGCTGT
TGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATCGCCCAAAA
GAACTTCATGAACATTTTGGAAAAAGTAGTACTGAAAGTTCTTGAAGACCA
GCAAAACATAAGACTCATACGGGAACTTCTCCAGACCCTCTACACATCCTT
ATGCACGCTGGTCCAGAGAGTCGGCAAGTCCGTGCTGGTGGGCAACATCAAC
ATGTGGGTGTATCGAATGGAGACCACTCTACACTGGCAACAGCAGCTGAACA
GCATCCAGATCAGCAGGCCGGCCTTCAAAGGTCTCACGATCACCGACCTGCC
TGTGTGCTTACAACTGAACATCATGCAGAGGCTGAGCGATGGGCGGGACCTG
GTCAGCCTGGGCCAGGCAGCCCCAGACCTGCATGTGCTCAGTGAAGACCGGC
TACTGTGGAAGAGACTCTGCCAGTACCACTTCTCAGAGCGGCAGATCCGCAA
GCGATTGATCTTGTCTGACAAAGGGCAGCTGGATTGGAAGAAGATGTACTTT
AAGCTTGTGCGATGTTACCCAAGAAGAGAACAGTATGGGGTCACCCTGCAGC
TTTGCAAACACTGCCACATTCTCTCCTGGAAGGGCACTGACCATCCATGCAC
GGCCAACAACCCAGAGAGCTGCTCCGTCTCACTTTCACCCCAAGACTTTATT
AACTTGTTCAAGTTC

Figure 11

MPFLGQDWRSPGQSWVKTADGWKRFLDEKSGTFVSDLSSYCNKENLFNSLNYD
VAAKKRKKDIQNSKTKTQYFHQEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAI
LDSRRFNYVVRLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNIRLIRELL
QTLYTSLCTLVQRVGKSVLVGNINMWVYRMETTLHWQQQLNSIQISRPAFKGLTI
TDLPVCLQLNIMQRLSDGRDLVSLGQAAPDLHVLSEDRLLWKRLCQYHFSERQIR
KRLILSDKGQLDWKKMYFKLVRCYPRREQYGVTLQLCKHCHILSWKGTDHPCTAN
NPESCSVSLSPQDFINLFKF

Figure 12

ATGCCATTCCTCGGGCAGGACTGGCGGTCCCCCGGGCAGAACTGGGTGAAGA
CGGCCGACGGCTGGAAGCGCTTCCTGGATGAGAAGAGCGGCAGTTTCGTGAG
CGACCTCAGCAGTTACTGCAACAAGGAGGTATACAATAAGGAGAATCTTTT
CAACAGCCTGAACTATGATGTTGCAGCCAAGAAGAGAAAGAAGGACATGCT
GAATAGCAAAACCAAAACTCAGTATTTCCACCAAGAAAAATGGATCTATGT
TCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTGGGGGAAGC
TTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC
TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGA
GTGGCATCGCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTTGA
AAGTCCTTGAAGACCAGCAAAACATTAGACTAATAAGGGAACTACTCCAGA
CCCTCTACACATCCTTATGTACACTGGTCCAAAGAGTCGGCAAGTCTGTGCT
GGTCGGGAACATTAACATGTGGGTGTATCGGATGGAGACGATTCTCCACTTGG
CAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTCAAAGGCCCTCA
CCTTCACTGACCTGCCTTTGTGCCTACAACTGAACATCATGCAGAGGCTGAG
CGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCTGCCCCCGACCTGCACGTGC
TCAGCGAAGACCGGCTGCTGTGGAAGAAACTCTGCCAGTACCACTTCTCCGA
GCGGCAGATCCGCAAACGATTAATTCTGTCAGACAAAGGGCAGCTGGATTTGG
AAGAAGATGTATTTCAAACTTGTCCGATGTTACCCAAGGAAAGAGCAGTAT
GGAGATACCCTTCAGCTCTGCAAACACTGTCACATCCTTTCCTGGAAGGGCA
CTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGCTCCGTTTCACTTTTG
A

Figure 13

SEQ. ID NO 10:

MPFLGQDWRSPGQNWVKTADGWKRFLDEKSGSFVSDLSSYCNKEVYNKENLFN
SLNYDVAAKKRKKDMLNSKTKTQYFHQEKWIYVHKGSTKERHGYCTLGEAFNRL
DFSTAILDSRRFNYVVRLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNI
RLIRELLQTLYTSLCTLVQRVGKSVLVGNINMWVYRMETILHWQQQLNNIQITRP
AFKGLTFTDLPLCLQLNIMQRLSDGRDLVSLGQAAPDLHVLSEDRLLWKKLCQYH
FSERQIRKRLILSDKGQLDWKKMYFKLVRCYPRKEQYGDTLQLCKHCHILSWKGT
DHPCTANNPESCSVSL

FIGURE 14

ClustalW Formatted Alignments

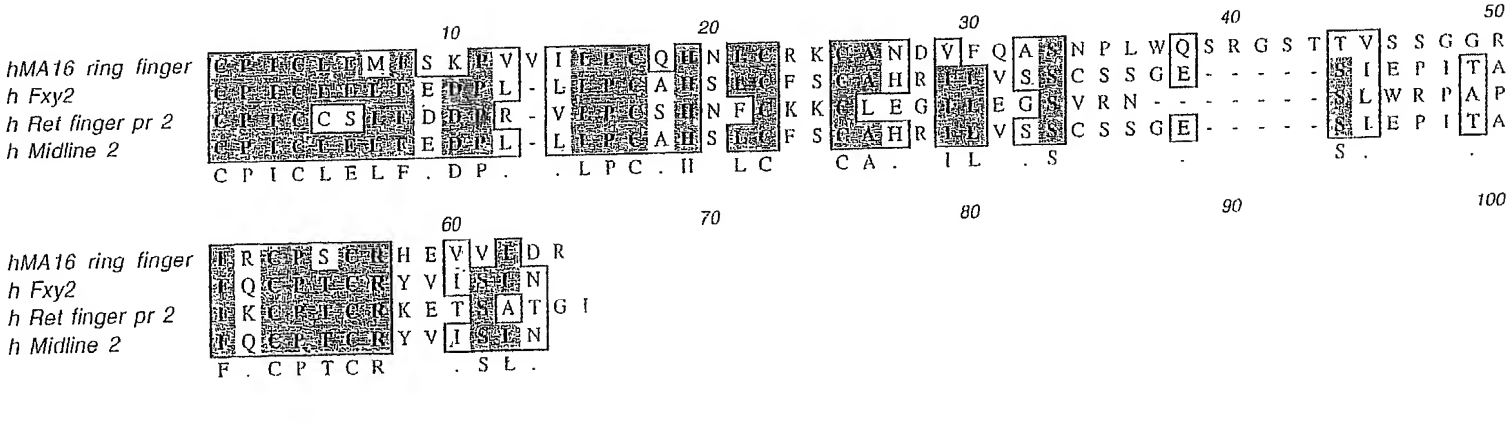

FIGURE 15

MA16 - A Monomeric Ring Ubiquitin Ligase

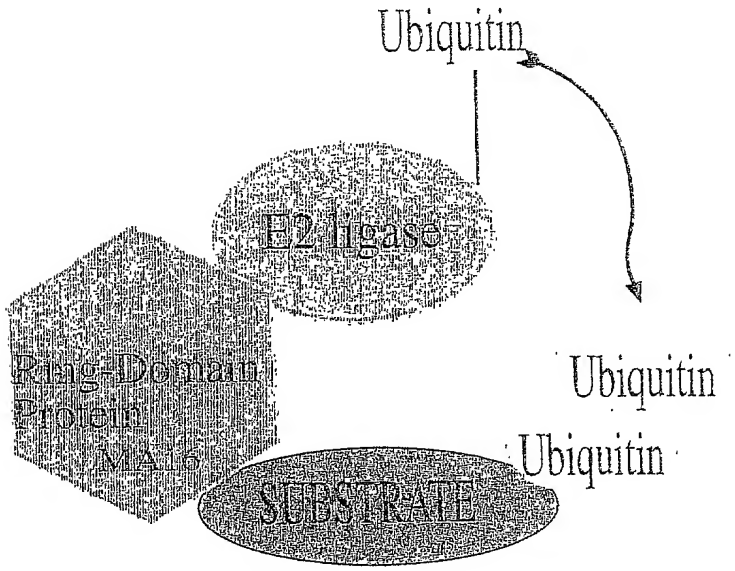

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Figure 16

ATGGACTACAAAGACGATGACGACAAAGATTATAAATCTGGCTTGATTCCG
GACGGAAATGCTATGGAGAACCTGGAGAAGCAGCTCATCTGCCCCATCTGCC
TTGAGATGTTTACCAAGCCTGTGGTCATCCTGCCCTGCCAGCACAACCTCTG
CCGGAAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTGGACCAAC
CGCGGTGGCTCGGTGTCCATGTCTGGAGGTCGTTTCCGCTGCCCCTCGTGCCG
CCATGAAGTGATCATGGACCGGCATGGGGTGTACGGTCTGCAGAGGAACCTG
CTGGTGGAGAACATCATCGACATCTACAAGCAGGAATGCTCCAGTCGGCCCC
TGCAGAAAGGCAGCCACCCGATGTGCAAGGAACACGAAGACGAGAAAATCA
ACATCTACTGTCTCACGTGCGAGGTGCCTACTTGCTCCTTGTGCAAGGTGTTC
GGGGCTCACCAGGCCTGTGAAGTTGCCCCCTTACAAAGCATCTTCCAAGGAC
AGAAGACTGAACTGAGCAATTGCATCTCCATGCTGGTGGCAGGGAACGACCG
AGTTCAGACTATCATCTCGCAGCTGGAGGACTCCTGCCGAGTGACCAAGGTG
AGGGTG

Figure 17

DYKSGLIPDGNAMENLEKQLICPICLEMFTKPVVILPCQHNLCRKCANDIFQAANP
YWTNRGGSVSMSGGRFRCPSCRHEVIMDRHGVYGLQRNLLVENIIDIYKQECSSR
PLQKGSHPMCKEHEDEKINIYCLTCEVPTCSLCKVFGAHQACEVAPLQSIFQGQK
TELSNCISMLVAGNDRVQTIISQLEDSCRVTKVRV

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Figure 18

ATGCCATTCCTCGGGCAGGACTGGCGGTCCCCCGGGCAGAACTGGGTGAAGA
CGGCCGACGGCTGGAAGCGCTTCCTGGATGAGAAGAGCGGCAGTTTCGTGAG
CGACCTCAGCAGTTACTGCAACAAGGAGGTATACAATAAGGAGAATCTTTT
CAACAGCCTGAACTATGATGTTGCAGCCAAGAAGAGAAAGAAGGACATGCT
GAATAGCAAAACCAAAACTCAGTATTTCCACCAAGAAAAATGGATCTATGT
TCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTGGGGGAAGC
TTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC
TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGA
GTGGCATCGCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGA
AAGTCCTTGAAGACCAGCAAAACATTAGACTAATAAGGGAACTACTCCAGA
CCCTCTACACATCCTTATGTACACTGGTCCAAAGAGTCGGCAAGTCTGTGCT
GGTCGGGAACATTAACATGTGGGTGTATCGGATGGAGACGATTCTCCACTGG
CAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTCAAAGGCCTCA
CCTTCACTGACCTGCCTTTGTGCCTACAACTGAACATCATGCAGAGGCTGAG
CGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCTGCCCCCGACCTGCACGTGC
TCAGCGAAGACCGGCTGCTGTGGAAGAAACTCTGCCAGTACCACTTCTCCGA
GCGGCAGATCCGCAAACGATTAATTCTGTCAGACAAAGGGCAGCTGGATTGG
AAGAAGATGTATTTCAAACTTGTCCGATGTTACCCAAGGAAAGAGCAGTAT
GGAGATACCCTTCAGCTCTGCAAACACTGTCACATCCTTTCCTGGAAGGGCA
CTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGCTCCGTTTCACTTTC
ACCCCAGGACTTTATCAACTTGTTCAAGTTC

Figure 19

MPFLGQDWRSPGQNWVKTADGWKRFLDEKSGSFVSDLSSYCNKEVYNKENLFN
SLNYDVAAKKRKKDMLNSKTKTQYFHQEKWIYVHKGSTKERHGYCTLGEAFNRL
DFSTAILDSRRFNYVVRLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNI
RLIRELLQTLYTSLCTLVQRVGKSVLVGNINMWVYRMETILHWQQQLNNIQITRP
AFKGLTFTDLPLCLQLNIMQRLSDGRDLVSLGQAAPDLHVLSEDRLLWKKLCQYH
FSERQIRKRLILSDKGQLDWKKMYFKLVRCYPRKEQYGDTLQLCKHCHILSWKGT
DHPCTANNPESCSVSLSPQDFINLFKF

Figure 20
ClustalW Formatted Alignments

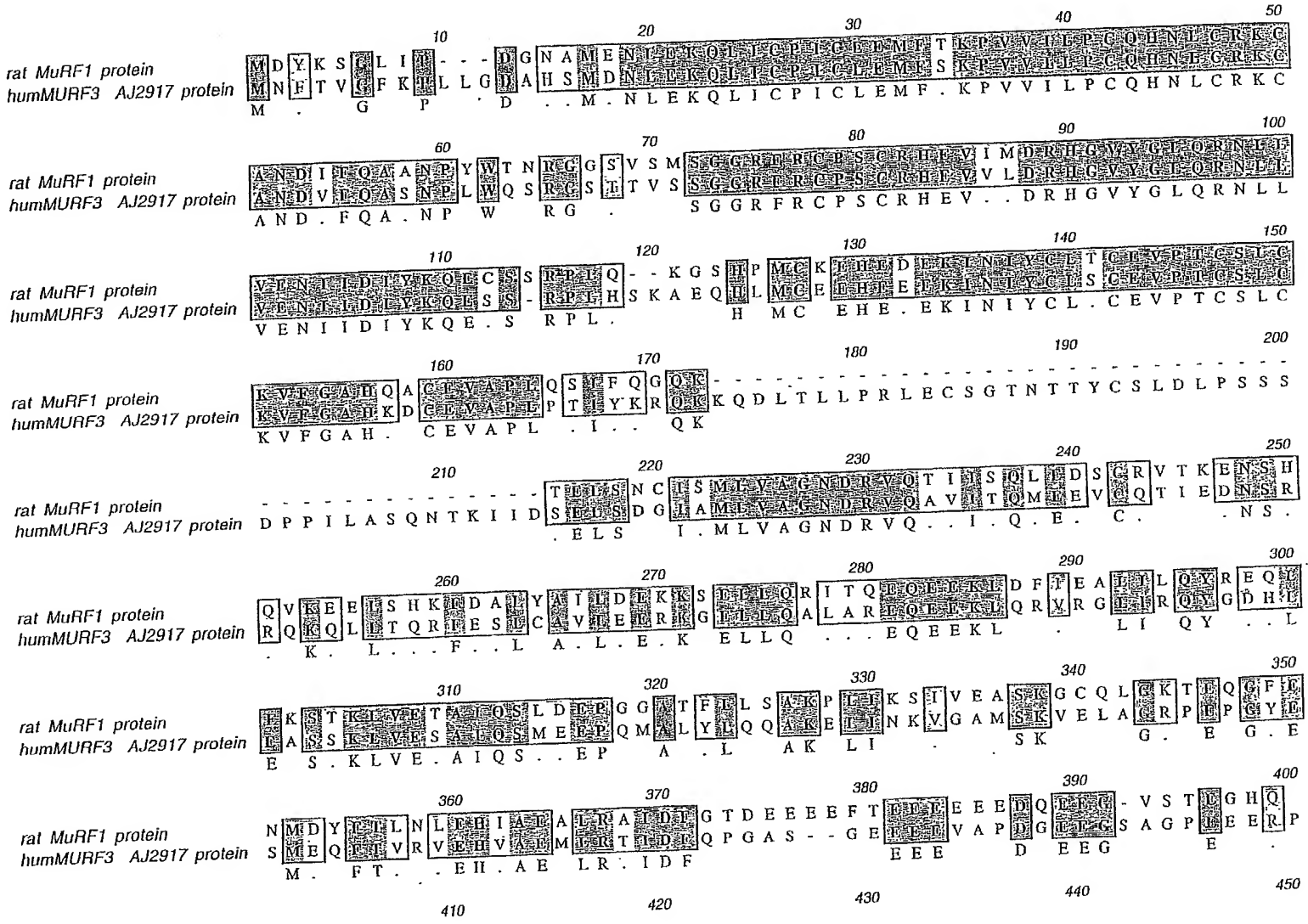


Figure 21

ATGAACTTCACAGTGGGTTTCAAGCCGCTGCTAGGGGATGCACACAGCATGG
ACAACCTGGAGAAGCAGCTCATCTGCCCCATCTGCCTGGAGATGTTCTCCAA
ACCAGTGGTGATCCTGCCCTGCCAACACAACCTGTGCCGCAAATGTGCCAAC
GACGTCTTCCAGGCCTCGAATCCTCTATGGCAGTCCCGGGGCTCCACCACTGT
GTCTTCAGGAGGCCGTTTCCGCTGCCCATCGTGCAGGCATGAGGTTGTCCTGG
ACAGACACGGTGTCTACGGCCTGCAGCGAAACCTGCTAGTGGAGAACATTTAT
CGACATTTACAAGCAGGAGTCATCCAGGCCGCTGCACTCCAAGGCTGAGCAG
CACCTCATGTGCGAGGAGCATGAAGAAGAGAAGATCAATATTTACTGCCTG
AGCTGTGAGGTGCCCACCTGCTCTCTCTGCAAGGTCTTCGGTGCCCACAAGG
ACTGTGAGGTGGCCCCACTGCCCACCATTTACAAACGCCAGAAGAGTGAGCT
CAGCGATGGCATCGCGATGCTGGTGGCAGGCAATGACCGCGTGCAAGCAGTG
ATCACACAGATGGAGGAGGTGTGCCAGACTATCGAGGACAATAGCCGGAGGC
AGAAGCAGTTGTTAAACCAGAGGTTTGAGAGCCTGTGCGCAGTGCTGGAGGA
GCGCAAGGGTGAGCTGCTGCAGGCGCTGGCCCGGGAGCAAGAGGAGAAGCTG
CAGCGCGTCCGCGGCCTCATCCGTCAGTATGGCGACCACCTGGAGGCCTCCTC
TAAGCTGGTGGAGTCTGCCATCCAGTCCATGGAAGAGCCACAAATGGCGCTG
TATCTCCAGCAGGCCAAGGAGCTGATCAATAAG

Figure 22

MNFTVGFKPLLGDAHSMDNLEKQLICPICLEMFSKPVVILPCQHNLCRKCANDVF
QASNPLWQSRGSTTVSSGGRFRCPSCRHEVVLDRHGVYGLQRNLLVENIIDIYKQ
ESSRPLHSKAEQHLMCEEHEEEKINIYCLSCEVPTCSLCKVFGAHKDCEVAPLPTI
YKRQKSELSDGIAMLVAGNDRVQAVITQMEEVCQTIEDNSRRQKQLLNQRFESLC
AVLEERKGELLQALAREQEEKLQRVRGLIRQYGDHLEASSKLVESAIQSMEEPQM
ALYLQQAKELINK

FIGURE 23

Table 1: Gene Transcripts Identified by the GeneTag™ Differential Display Method

Up-regulated Genes

MA1	+4x	KIAA1401
MA2	+3x	Novel, similar to dbEST 7148688
MA3	+10x	Histone deacetylase 4
MA5	+3x	AK023151
MA6	+3x	AW91013 (has UBX domain)
MA10	+3x	Acyl-CoA dehydrogenase
MA11	+3x	Stat5b
MA12	+6x	AML1
MA14	+5x	PC3
MA15	+3x	MAC30
MA16	+4x	**MuRF1**
MA17	+4x	Novel, similar to dbEST Id: 5089799
MA22	+10x	SUMIKO; Intermediate filament pro.
MA24	+3x	Hsp 86
MA25	+3x	26s proteasome regulatory subunit
MA27	+11x	p21 cyclin-dependent kinase inhibitor
MA28	+3x	KIAA1370
MA30	+4x	LIFR, membrane-bound, alpha chain
MA35	+8x	= MA61 = MAFbx
MA37	+10x	Acetylcholine receptor, alpha subunit
MA39	+7x	mCARP
MA43	+3x	CD24 heat stable antigen; nectadrin
MA51	+3x	BC004765; band 4.1 homology
MA52	+5x	Osteoactivin nmb
MA53	+5x	Novel, dbEST Id: 1797808
MA55	+3x	K009425, SEC24 related
MA56	+5x	BC012075 similar to beta-transducin
MA58	+3.6x	Novel, dbEST Id: 4658995
MA59	+3x	Novel, dbEST Id: 2364370 similar to rev7, MAD
MA61	+8x	**MAFbx**
MA65	+3x	TAZ
MA66	+2.5x	polyubiquitin
MA67	+3.1x	5'-AMP-activated protein kinase beta subunit
MA72	+5.9x	PA28 beta

Down-regulated Genes

MA4	-3x	Novel, dbEST Id: 3180495
MA7	-3x	delta subunit of F1F0ATPase
MA8	-3x	X-chromosome linked phosphoglycerate kinase
MA9	-3x	Myotilin
MA13	-3x	PTP H1
MA18	-3x	HSKM-B
MA19	-3x	Voltage-gated Ca++ channel a2/delta subunit
MA20	-3x	AK021835
MA21	-3x	MGST3
MA23	-4x	Pyruvate kinase M1 and M2 subunit
MA26	-4x	Novel, dbEST Id: 2126427
MA29	-3x	myosin-binding protein C, fast type muscle
MA31	-4x	skelemin, myomesin
MA32	-3x	Novel, dbEST Id 4667680
MA33	-3x	Novel
MA34	-10x	Fructose 1,6 biphosphatase
MA36	-3x	Cypher
MA38	-5x	MCT3
MA40	-3x	osteonectin/SPARC
MA41	-3x	tropomyosin, skeletal muscle beta
MA44	-3x	Lactate dehydrogenase
MA45	-3x	Adenylosuccinate synthase
MA46	-3x	Phosphoglycerate mutase
MA47	-4x	phosphofructokinase
MA48	-2x	UDP-glucose pyrophosphorylase
MA49	-3x	aralar1
MA50	-3x	F1-ATPase alpha subunit
MA54	-2.8x	ZIP
MA60	-3.2x	Creatine Kinase
MA64	-4.5x	early gene transcription factor NGF1-B RNA
MA68	-5.9x	lactate dehydrogenase
MA71	-4x	betaPix
MA73b	-3x	Net1
MA75	-2x	Myosin light chain 2

FIGURE 24

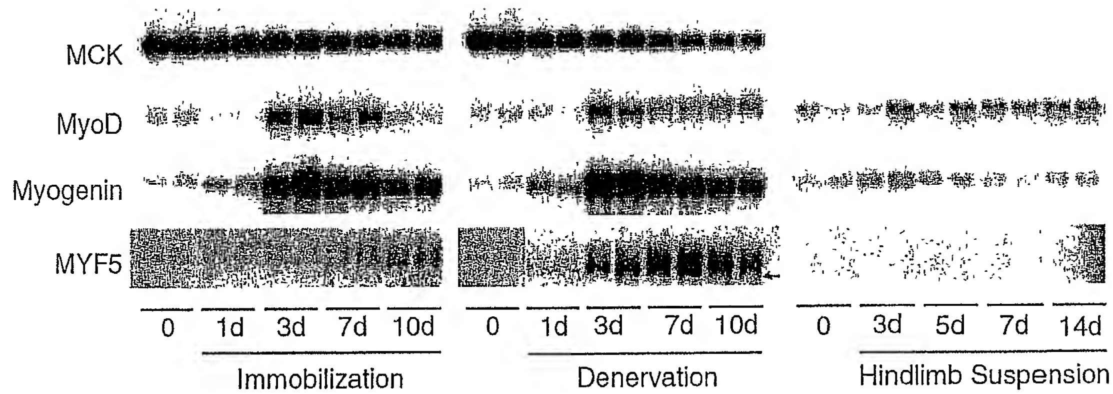
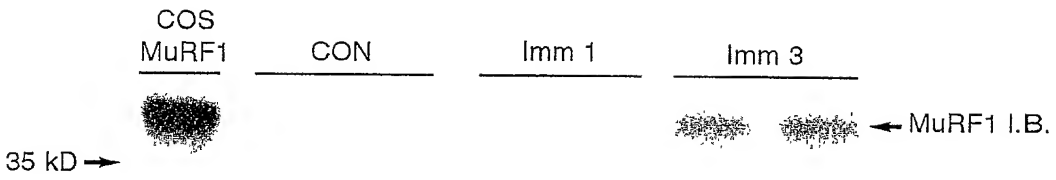
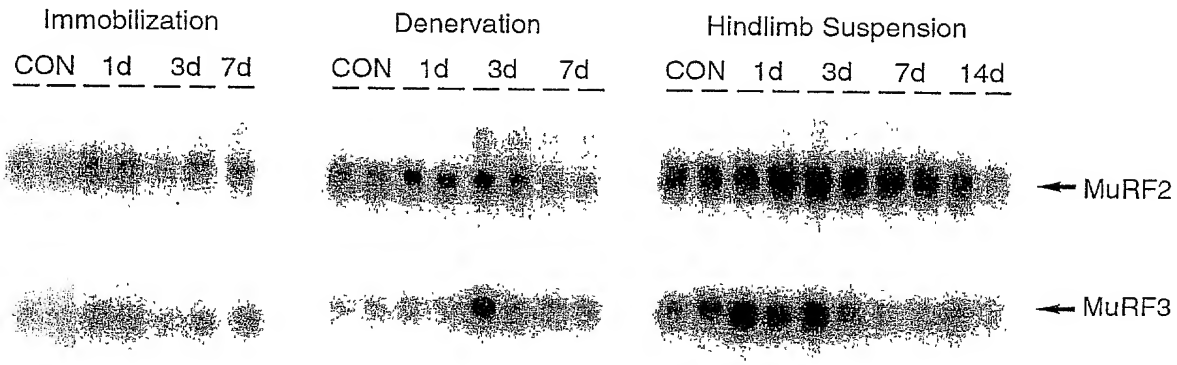

MCK
MyoD
Myogenin
MYF5
0
1d
3d
7d
10d
Immobilization
0
1d
3d
7d
10d
Denervation
0
3d
5d
7d
14d
Hindlimb Suspension

FIGURE 25A



I.P.: Anti-MuRF1

FIGURE 25B



SUBSTITUTE SHEET (RULE 26)

FIGURE 26

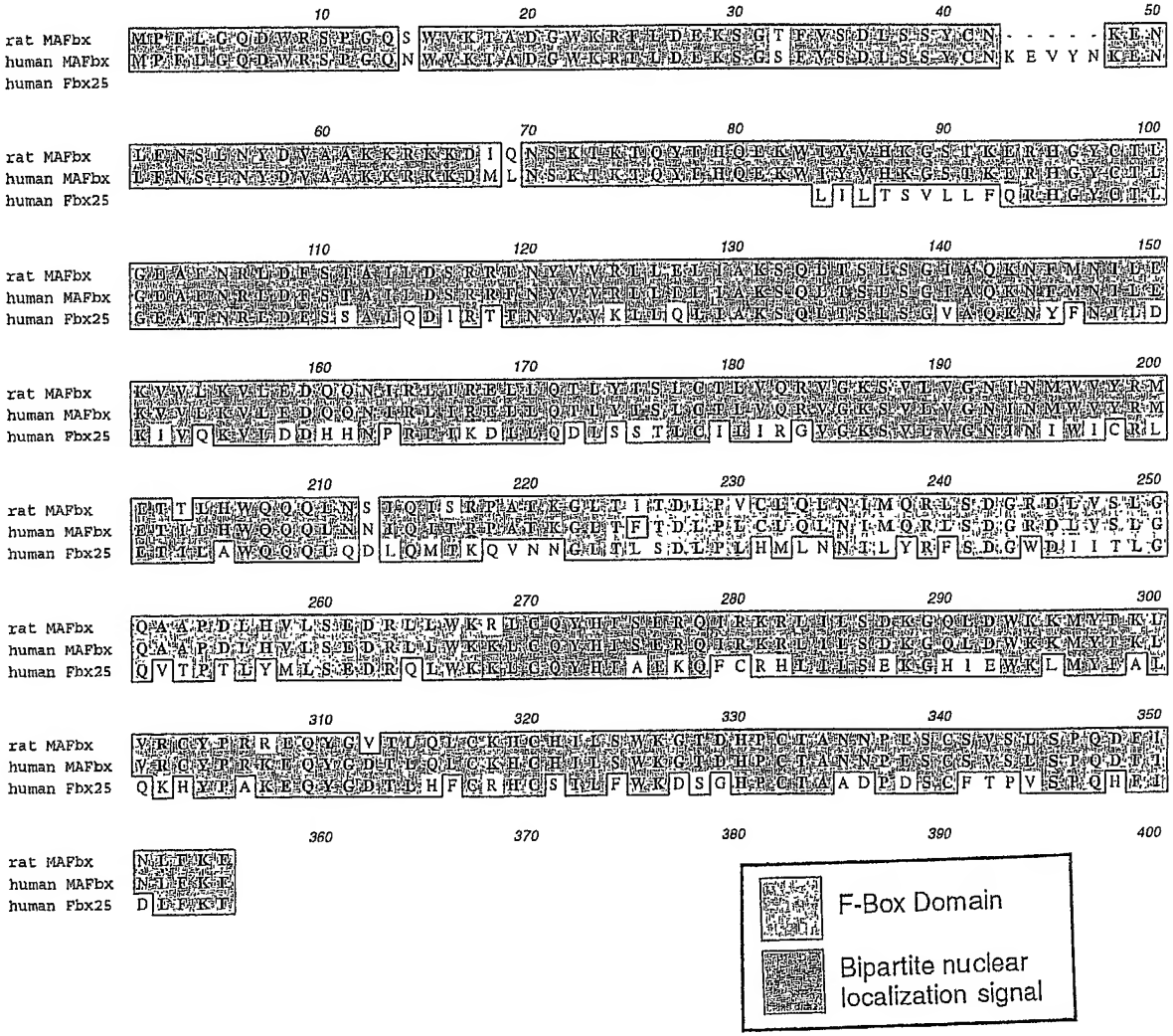

rat MAFbx
human MAFbx
human Fbx25
F-Box Domain
Bipartite nuclear localization signal

FIGURE 27A

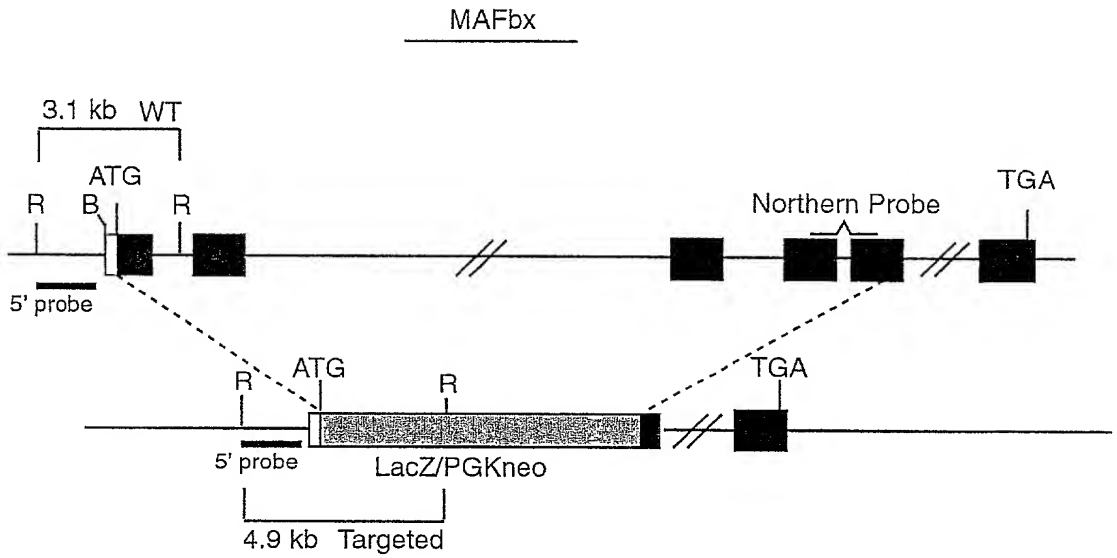


FIGURE 27B

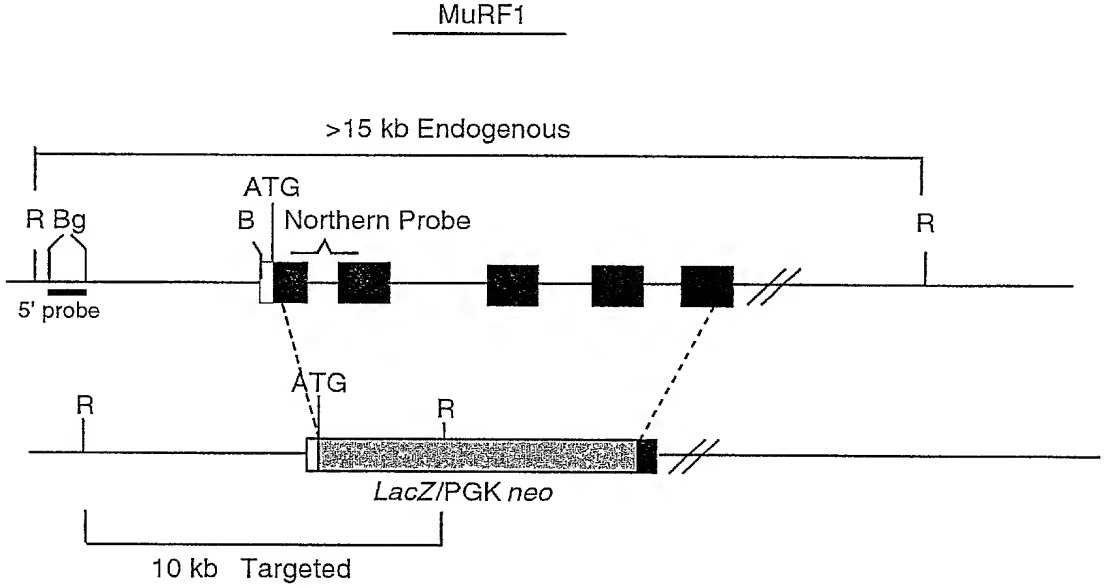


FIGURE 28A

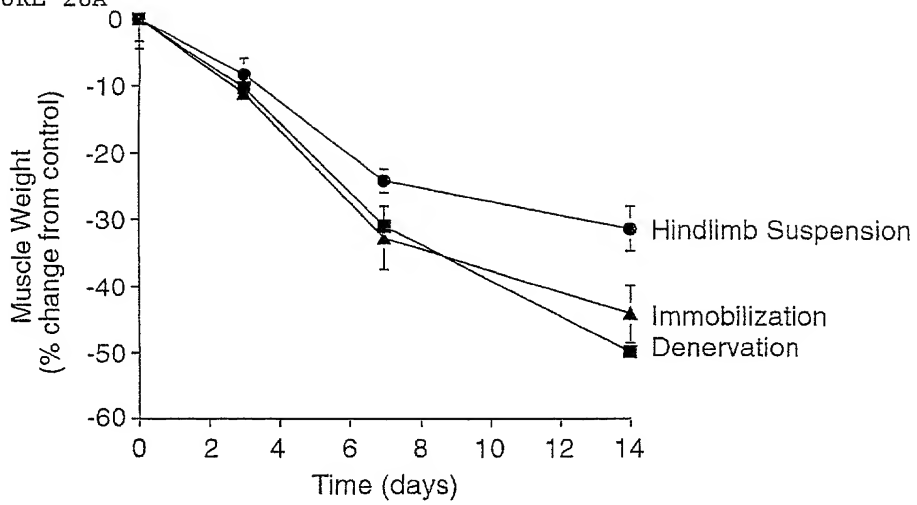


FIGURE 28B

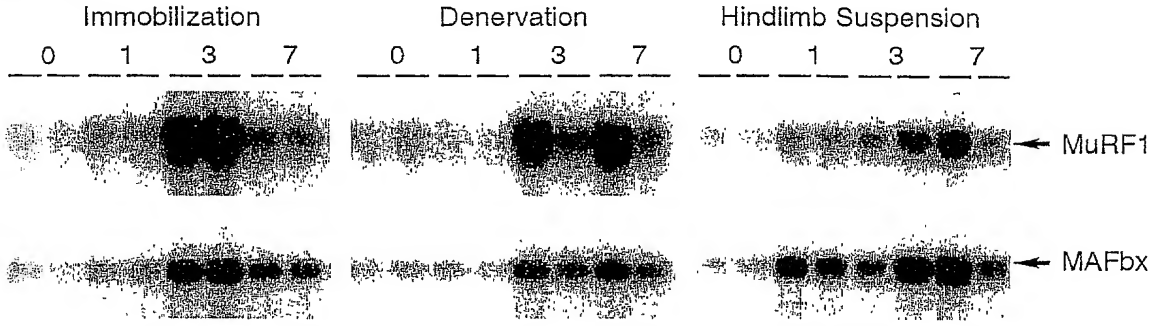


FIGURE 28C

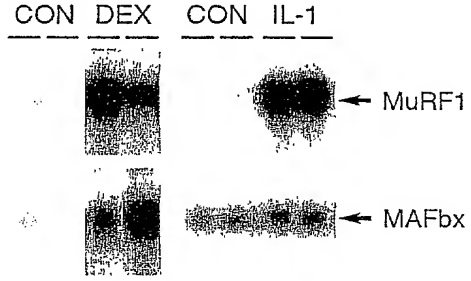


FIGURE 28D

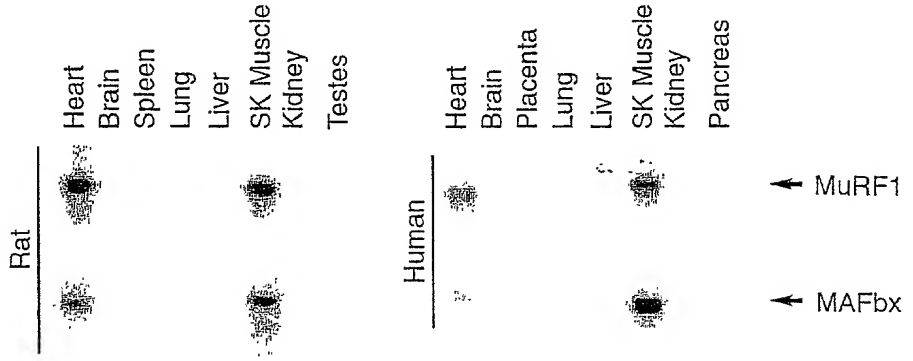


FIGURE 29A

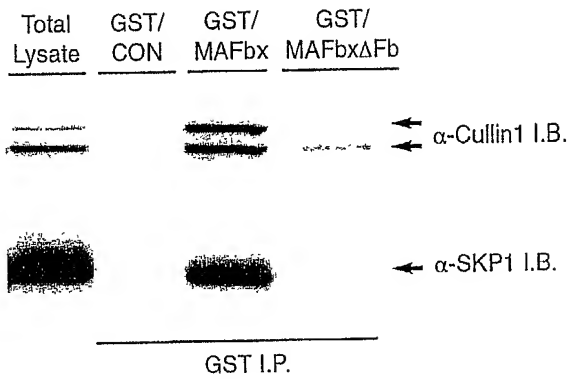


FIGURE 29B

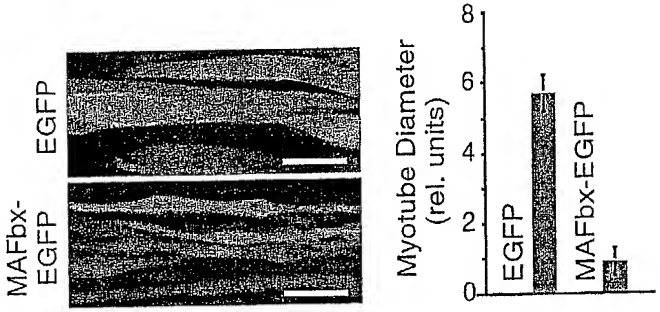


FIGURE 29C

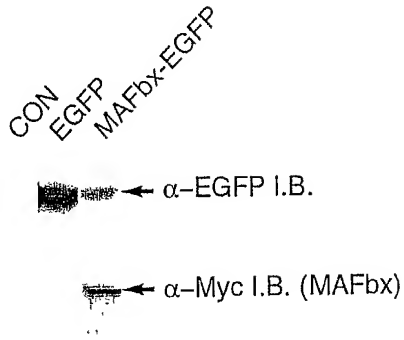


FIGURE 29D

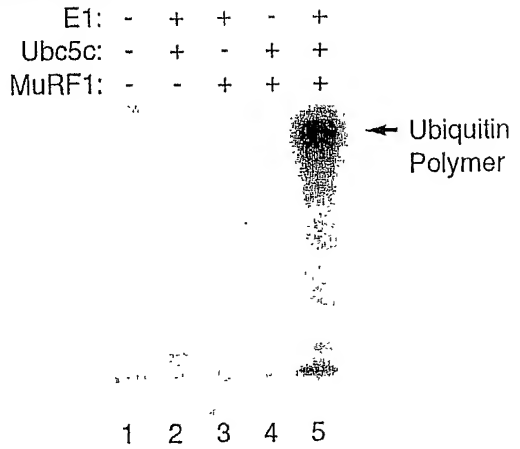


FIGURE 30A

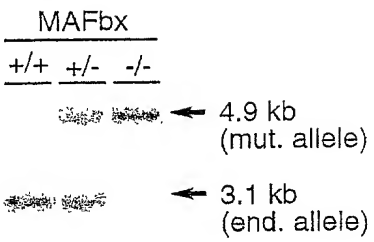


FIGURE 30C

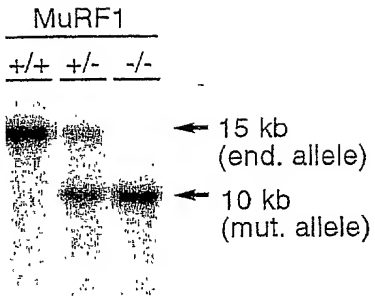


FIGURE 30B

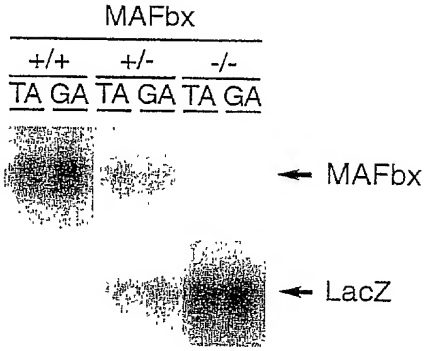


FIGURE 30D

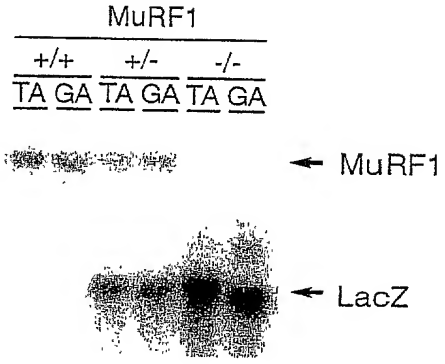
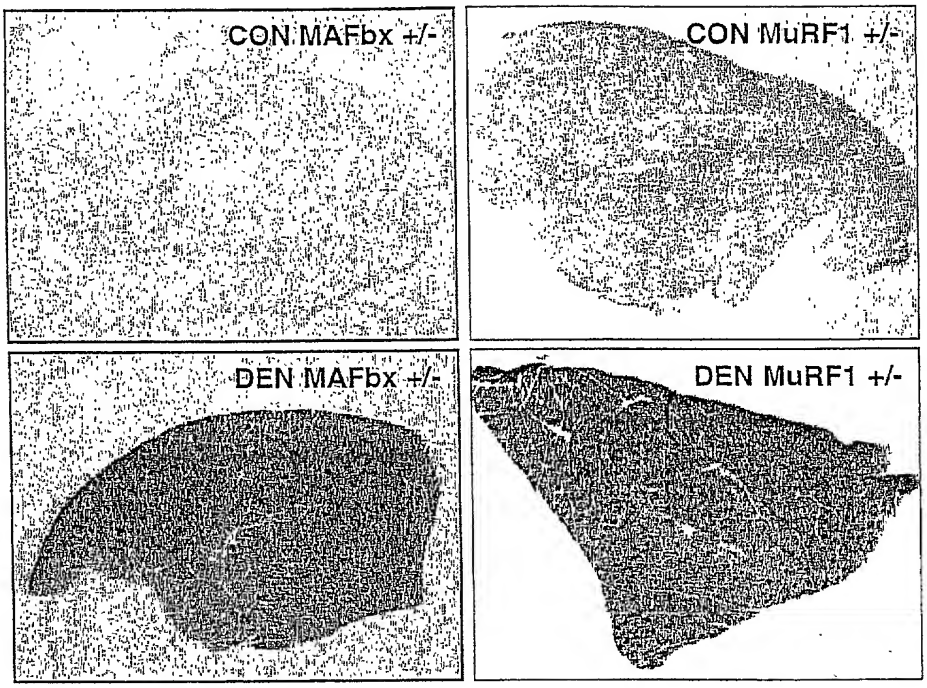


FIGURE 31A



FIFURE 31B

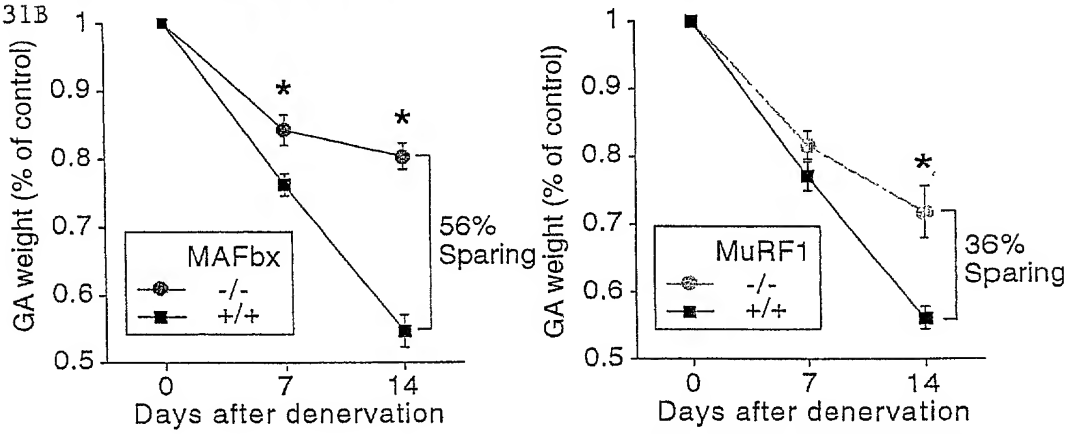


FIGURE 31C

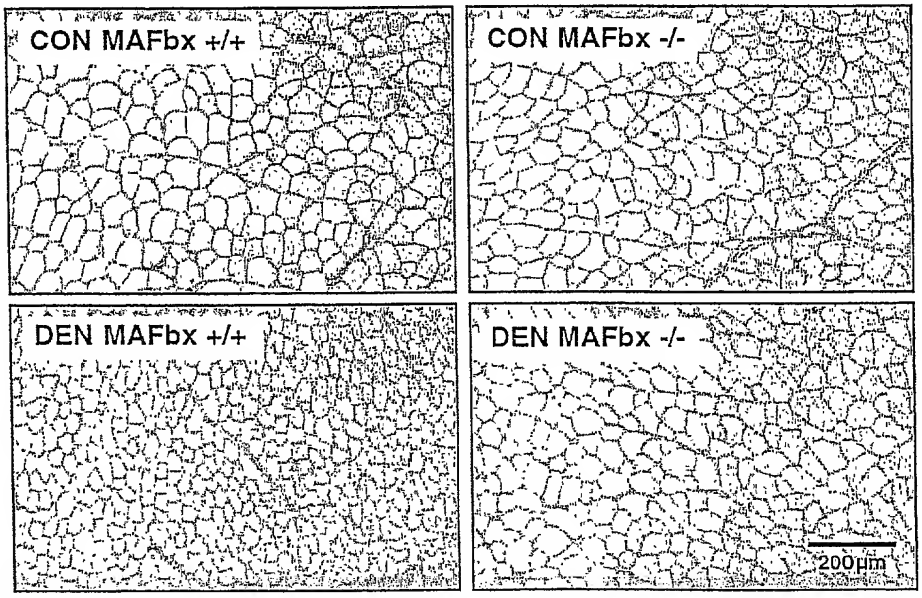


FIGURE 32

ClustalW Formatted Alignments

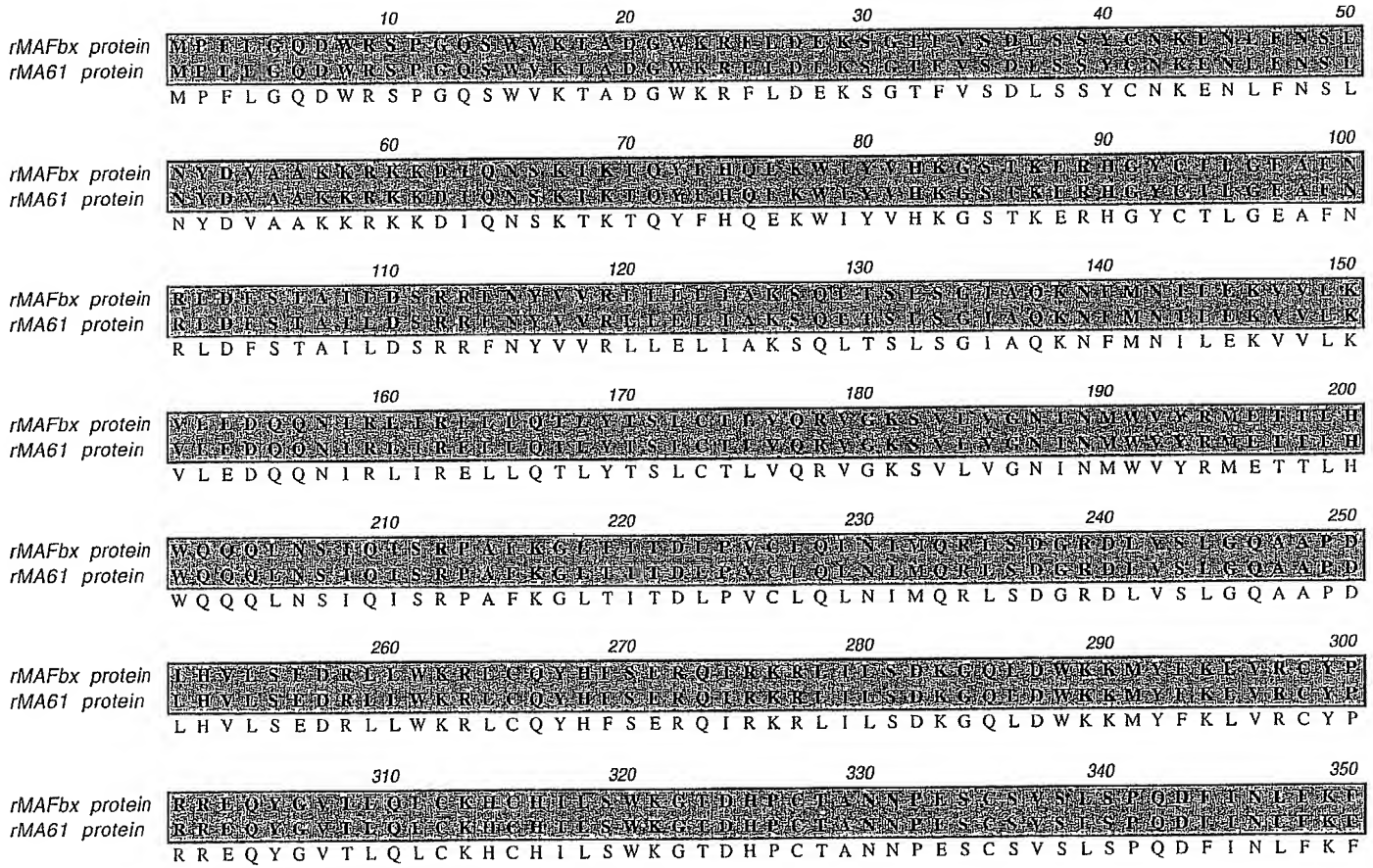


FIGURE 33

ClustalW Formatted Alignments

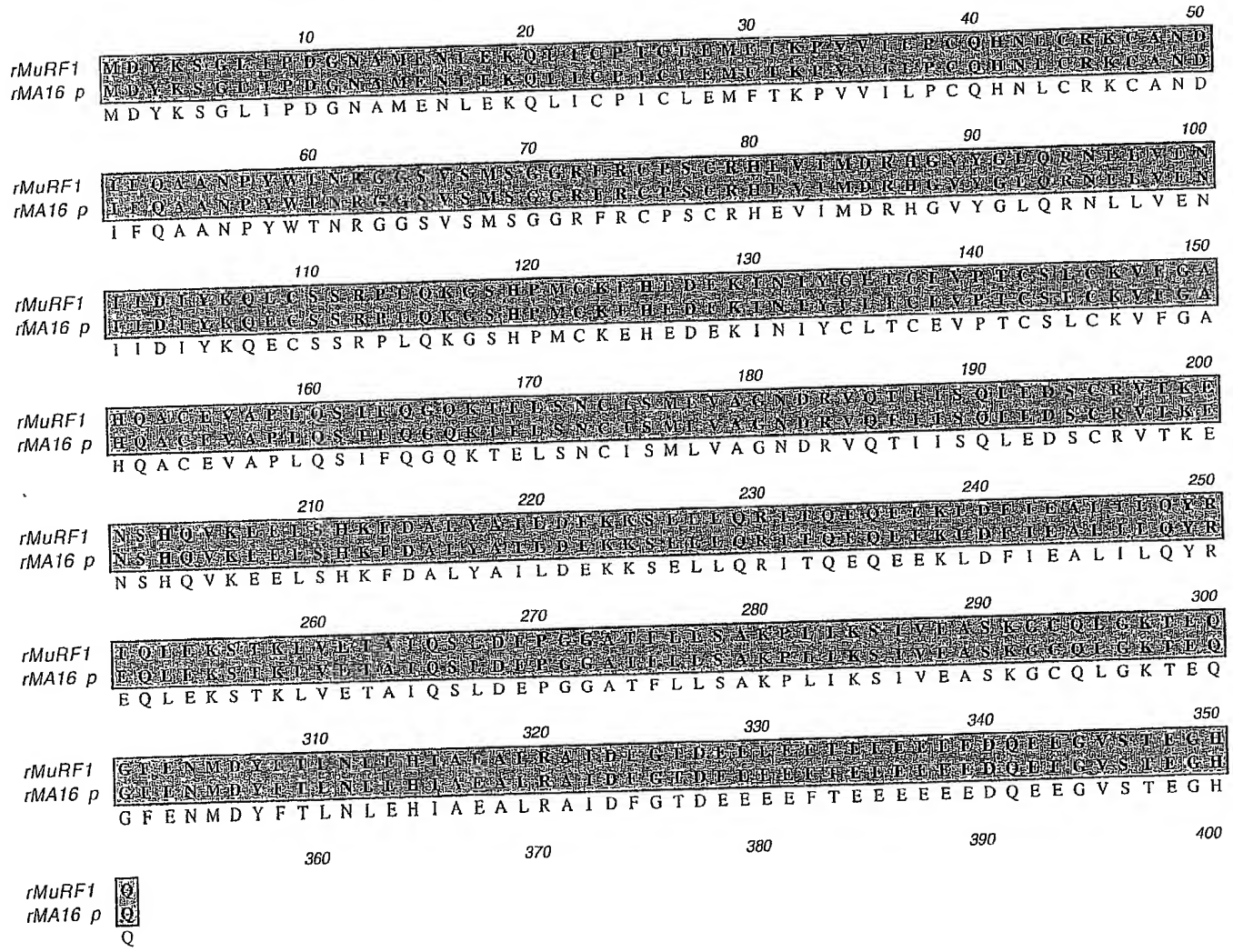


Figure 34
ClustalW Formatted Alignments

```
                                10                  20                  30                  40                  50
rMA16 protein       M D Y K S G L I P D G N A M E N L E K Q L I C P I C L E M F T K P V V I L P C Q H N L C R K C A N D
humMURF1 protein    M D Y K S S L I Q D G N P M E N L E K Q L I C P I C L E M F T K P V V I L P C Q H N L C R K C A N D
                    M D Y K S   L I   D G N   M E N L E K Q L I C P I C L E M F T K P V V I L P C Q H N L C R K C A N D

                                60                  70                  80                  90                  100
rMA16 protein       I F Q A A N P Y W T N R G G S V S M S G G R F R C P S C R H E V I M D R H G V Y G L Q R N L L V E N
humMURF1 protein    I F Q A A N P Y W T S R G S S V S M S G G R F R C P T C R H E V I M D R H G V Y G L Q R N L L V E N
                    I F Q A A N P Y W T   R G   S V S M S G G R F R C P . C R H E V I M D R H G V Y G L Q R N L L V E N

                                110                 120                 130                 140                 150
rMA16 protein       I I D I Y K Q E C S S R P L Q K G S H P M C K E H E D E K I N I Y C L T C E V P T C S L C K V F G A
humMURF1 protein    I I D I Y K Q E C S S R P L Q K G S H P M C K E H E D E K I N I Y C L T C E V P T C S M C K V F G I
                    I I D I Y K Q E C S S R P L Q K G S H P M C K E H E D E K I N I Y C L T C E V P T C S . C K V F G

                                160                 170                 180                 190                 200
rMA16 protein       H Q A C E V A P L Q S I F Q G Q K T E L S N C I S M L V A G N D R V Q T I I S Q L E D S C R V T K E
humMURF1 protein    H K A C E V A P L Q S V F Q G Q K T E L N N C I S M L V A G N D R V Q T I I T Q L E D S R R V T K E
                    H . A C E V A P L Q S . F Q G Q K T E L   N C I S M L V A G N D R V Q T I I . Q L E D S   R V T K E

                                210                 220                 230                 240                 250
rMA16 protein       N S H Q V K E E L S H K F D A L Y A I L D E K K S E L L Q R I T Q E Q E E K L D F I E A L I L Q Y R
humMURF1 protein    N S H Q V K E E L S Q K F D T L Y A I L D E K K S E L L Q R I T Q E Q E E K L S F I E A L I Q Q Y Q
                    N S H Q V K E E L S . K F D . L Y A I L D E K K S E L L Q R I T Q E Q E E K L   F I E A L I   Q Y .

                                260                 270                 280                 290                 300
rMA16 protein       E Q L E K S T K L V E T A I Q S L D E P G G A T F L L S A K P L I K S I V E A S K G C Q L G K T E Q
humMURF1 protein    E Q L D K S T K L V E T A I Q S L D E P G G A T F L L T A K Q L I K S I V E A S K G C Q L G K T E Q
                    E Q L . K S T K L V E T A I Q S L D E P G G A T F L L . A K   L I K S I V E A S K G C Q L G K T E Q

                                310                 320                 330                 340                 350
rMA16 protein       G F E N M D Y F T L N L E H I A E A L R A I D F G T D E E E E - F T E E E - - E E E D Q E E G V S T
humMURF1 protein    G F E N M D F F T L D L E H I A D A L R A I D F G T D E E E E E F I E E E D Q E E E E S T E G K - E
                    G F E N M D . F T L   L E H I A . A L R A I D F G T D E E E E   F   E E E     E E E .     E G

                                360                 370                 380                 390                 400
rMA16 protein       E G H Q
humMURF1 protein    E G H Q
                    E G H Q
```